Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. • n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu May 6 15:08:47 1999; MasPar time 1644.23 Seconds 1384.282 Million cell updates/sec

Tabular output not generated. Run on:

>US-09-037-460-1 (1-1271) from US09037460.seq 1266 Title: Description: Perfect Score: N.A. Sequence: Comp:

1 CTGCTTCCCACCAGCAAGA......GTTNCCTNTNTCTNAAGGAC 1271
GACGAAGGGTGGTCGTTTCT......CAANGGANANAGANTTCCTG

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

2275026 seqs, 895388244 bases x 2 Searched:

Minimum Match O% Listing first 45 summaries Post-processing:

embl-est56 Database: Database:

l:em_estl 2:em_gssl 3:em_gss2 4:em_gss3
genbank-estl09
5:gb_estl 6:gb_estl0 7:gb_estl1 8:gb_estl2 9:gb_estl3
10:gb_estl4 11:gb_estl5 12:gb_estl6 13:gb_estl7
14:gb_estl8 15:gb_estl9 16:gb_est2 17:gb_estl7
18:gb_estl1 19:gb_est8 20:gb_est4 21:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_est6
28:gb_gss3 29:gb_gss4

Mean 11.873; Variance 3.231; scale 3.674 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

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ALIGNMENTS

1 425 bp mRNA EST 11-OCT-1996 c233e02.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA W46667 9131295	<pre>human. human. Homo sapiens Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 425) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rutchan,M., Rutchan,M., Rutchan,M., Soares,M., Tennon,G., Marra,M., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.</pre>	The Washu-Merck EST Project Unpublished (1995) Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Porest Park Parkey Box 8501, St. Louis, MO 63108 Fax: 314 286 1810	Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the InAGE Consortium (info@image.llnl.gov) for further information. Inagert Length: 132
TION ION DS	SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES

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Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkess,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Bandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA296697 351 bp mRNA EST 18-APR-1997 EST112419 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end similar to endothelial cell-specific secretory molecule, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AAGCTGAAGACCGCAGTGAGTCAAATTAGTTCTTTGACTTTGATGTACATTAATGTTGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                          181 ATATGGAATGAAGACTTAAGAGCAGGAGANGATGGNNAGGGGGGTGGGAGTGGGAAATAAA 240
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                                                                                                       /clone="324122"
/clone_lib="Soares senescent fibroblasts NbHSF"
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                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                    Length 425;
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Pred. No. 0.00e+00;
2; Mismatches 5; Indels
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larity 98.1%;
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Kelley, J.W., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Ho, W., Hu, J.S., Greens, J.M., Fischer, C., Hastings, G.A., Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Paymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Paymond, L., Rennon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bloinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavefigr.org
Email: arkerlavefigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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AA754459 92801165
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1 (Dases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
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/note="Organ: aorta; Vector: pBluescript
ScoR; Site_2: XhoI"
/db_xref="ATCC (inhost):115698"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 others
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Pred. No. 1.44e-152;
1; Mismatches 8;
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/cell_type="endothelial cell"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                 Other_ESTs: THC154673
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llarity 94.0%;
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TITLE JOURNAL COMMENT

source

FEATURES

BASE COUNT

ORIGIN

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/organism="Oryza sativa"
/organism="Oryza sativa"
/oultivar="Milyang23"
/oultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI: Directional cDNA library inserted into lambda ZAPII
Vector at 5'end with EcoRI and 3' end with Xho I site."
/db.ref="Laxon:4530"
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/dev_stage="5 days after pollination"
/lab_host="Ecoli SOLR"
/ lab_host="Ecoli Solr"
/ lab_host="
                             Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Tex: 82 331 290 0307
Email: 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Basek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Rorea. 449-728 bhnahm@bioserver.myongji.ac.kr
Location/Qualifiers
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Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Basek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserVer.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Bahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 DWHYWBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCM 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCIMWCWBHYNTKCTASGWHTSINYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 BAWMITSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSG
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4.4%; Score 56; DB 12; Length 252
Best Local Similarity 9.6%; Pred. No. 6.87e-37;
Matches 21; Conservative 111; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 ITRAIRSYICVRKYCVMWMIKKVVKKYHVVBBGCHBIDS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 AACACTGAAGAACTAAAAATGCAATTTAGGTAATCTTAC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Eun M.Y.
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1: Directional cDNA library inserted into lambda ZAPII
Xho2: Tat 5 end With EcoRI and 3' end With Xho I site."
/db_xref="taxon:4530"
/clone="978N1787"
/clone="1p="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
5 a 21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                        Email: myeun@suz20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence. AA754459 92801165
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1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 GNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTKC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 CACTCCCACCCCTCCCCATCTTCTCCTGCTCTAAGTCTTCCATATCCCAACATT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 TASGWHTSTNYDVKSSTNT-WGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 VWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 252;
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Best Local Similarity 11.3%; Pred. No. 1.37e-44;
Matches 23; Conservative 107; Mismatches 71; Indels
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National Inst. of Agri. Sci. and Tech, RDA
                                                                                                                                                                        Department of Cytogenetics
National Inst. of Agri. Sci. and Tech,
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 YCVMWMTKKVVKKYHVVBBGCHB 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
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LOCUS DEFINITION

RESULT

ACCESSION

923

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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1600 MTKRYYRYSWTGWTKWTTWWYMWSMTRW 1627
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ORGANISM
                                                                       BASE COUNT
ORIGIN
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AUTHORS
TITLE
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                                                  /organism="Oryza sativa"
/cultivar="Milyang33"
/cultivar="Milyang33"
/cultivar="Milyang33"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional cDNA library inserted into lambda ZAPII
Vector at 5'end with EcoRI and 3' end with XhO I site."
/db.xref="Laxon:4530"
/clone="97SN1784"
/clone="57SN1784"
/clone="67SN1784"
/clone="67SN1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458 92801164
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Bukaryotaes; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta: Tracheophyta; seed plants; Magnollophyta; Liliopsida;
Poales; Poaceae; Oryza.
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Subaitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 247)
Nahm, B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Rang,R.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 VWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTS-ATKRVTGYDKTDSDCGGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 CAACACTGTGACAGCAGTGAGTGCAAAAGCAGCCCGCGCTGCAAGAGGACAGTGCTCGAC 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $ :::| |::::| ::::| 205 GACTGTGCTGCTGCTGCGGGGGGGGAGAA-ACTTGCTACCGCACAG 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 247;
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Pred. No. 5.86e-27;
89; Mismatches 65; Indels
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National Inst. of Agri. Sci. and Tech, 1
Suwon, Kyungdido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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/organism="Oryza sativa"
/cultivar="Milyang23"
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Local Similarity 12.8%;
les 23; Conservative
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                                 source
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ORIGIN
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JOURNAL
COMMENT
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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2 (bases I to 2275)
Tripodls, N. and Ragoussis, J.
Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2275 bp mRNA EST 22-DEC-1997
ntcon2 contig mRNA, partial sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1481 YKRWKRKGRRKRWIGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYIST 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1267 TINAGANANAGGNAACCCGGGGGCTACATCAGCAGCCTTTTGRAATTGCTC-TCAGNTCA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1541 YYKSWSRWYWTTYTYWYCWCCTSMKSASCA-MMRWMGYMGSRSSRSYWGYWGSMSGCYG 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1208 AAGCIGITIGITACICAAAITICCATAAGCITCAAAACAICITACITCCTICAGGGGITIT 1149
                                                                                                                                                                                                                                                                               76 GYGTBYYSWNVDINTGGTGVGKTIVNVHSGWNNRCSNSVVYVWBIAYCDYBHYBDRANHV 135
                                                                                                                                                                                                                                                                                                                                                                                          136 DDTRCINDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCCGGCAGCATTCTCTT-TCACAACTTCTCTCTA--CAATATTGCCATCTCCAGAT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                             16 CBAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKY 75
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2275)
Tripodis, " and Ragoussis, J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 11; Length 2275;
Pred. No. 5.24e-12;
80; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCATGTCGTCGTGAGAAAAAAAATCTGTTGGAAGACTTGGTTA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 VRITSMWIDKSIKMBSMDMSRRSRVHYGRWMBNKKRCMSRNWIDIKIWR 244
                                                                                                                                          Length 247;
                                                           169 others
                                                                                                                                 Query Match
3.6%; Score 46; DB 12; Length 247
Best Local Similarity 11.4%; Pred. No. 1.51e-24;
Matches 26; Conservative 112; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 others
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 ot:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       599 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="liver; brain"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"similar to Br140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ntcon2 contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 g
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; I primates; Catarrhini; Hominidae; Homo.

(bases 1 to 467)

Mahairas,G., Wallace,J.C., Smith,K., Swartzell,B., Furlong,J., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    raszo494 199 bp mRNA EST 21-APR-1998 Crust cDNA Library Trypanosoma AA926494 GONE 1116 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
/db_xref="taxon:9606"
/clone="Plate=3095 Col=8 Row=M"
/clone=lib="CIT Approved Human Genomic Sperm Library D'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)
Av. Gral Paz entre Albarellos y Constituyentes, INTI edifício 24 Cp(1650) San Mattin, Prov. de BS. Argentina
Tel: (54-1)752-9639 or (54-1)752-0021
Fax: (54-1)752-0021 or (54-1)752-9639
Email: dsanchez@inti.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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1 (bases 1 to 199)
Verdun, R.E., D1 Paolo, N.C., Rondinelli, E., Frasch, A.C.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing in Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallacedu.washington.edu
Sequence Tagged Connector
Sequence Tagged Connector
Plate: 3095 row: M column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 7.59e-07;
0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1072 AGGTAGCITCICTAGAAITIAAITRIGCITITITITITITIT 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 467 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 g
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Gene discovery through EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
72 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7. Match
Local Similarity 39.4%;
les 41; Conservative
                                                                                                                                                                                                                                                                                                                        Sequencing
Unpublished (1998)
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                                                                                                                 Homo sapiens
                                                     GSS.
human.
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AUTHORS
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                                               KEYWORDS
SOURCE
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Matches
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JOURNAL
COMMENT
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KEYWORDS
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B
                                                                                                                              AMA/U2386 236 bp mRNA EST 19-DEC-1997
2f90b06.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 384179
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //OCE-"OTGEN: OFFICE OF THE STATE OF THE STATE OF THE STATE OF STA
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryofde; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Pirnates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 236)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Marian, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089 TITAATIRIGCITITITITITITITIGGGCTITIGGGAAAGICAAAATAAAACAACCAG 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
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Pred. No. 6.83e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:1299436"
/db_xref="taxon:9606"
/clone="384179"
/clone=lib="Soares pineal gland N3HPG"
/lab_host="DH10B (ampicillin resistant)"
a 47 c 22 g 100 t
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Contact: Wilson RK

TITLE JOURNAL COMMENT

source

FEATURES

Homo sapiens

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

92705499 human.

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RESULT

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DEFINITION

ACCESSION

Oudry Match
Best Local Similarity 75.4%;
Matches 49; Conservative

67

BASE COUNT

ORIGIN

AQ151727 93540775

ACCESSION NID

1149 AAAAC 1153

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RESULT

LOCUS

168 GAAAC 172

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/clone-"IMAGE:1637415"
/clone_lib-"NCI_CGAP_GC3"
/tissue_type-"pooled germ cell
/lab_host-"DH10B"
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g
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                                                                                                                                                                                                                                                            Query Match 2.3%;
Best Local Similarity 80.9%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3%;
Best Local Similarity 79.2%;
Matches 38; Conservative
                                                                                                                                                                    63
C
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Trypanosoma cruzi
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AA642307
92567525
EST.
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                                                                                                        /organism="Trypanosoma cruzi"
/strain="Cl-Brenner"
/strain="Cl-Brenner"
/strain="Cl-Brenner"
/strain="Cl-Brenner"
/strain="Cl-Brenner"
/strain="Cl-Brenner"
/stone="Instrain organism organism of the path of the proper organism or
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Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E
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/organism="Homo sapiens"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker: lst strand cDNA was prepared from 3 pooled
germ cell tunors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Ec
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="texon:8606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovisf08.si NCI_GGAP_GC3 Homo sapiens cDNA clone IMAGE:1637415 3/
similar to TR:016465 Q16465 367BP EXPRESSED SEQUENCE TAG MRNA ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncb1.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 199;
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 14;
Pred. No. 7.20e-06;
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Best Local Similarity 72.6%;
Matches 45; Conservative
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Unpublished (1997)
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AI005619
g3215129
                          primer: T7
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/note="cDNA library constructed with oligo dT primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker (PHARMACIA)"
/db.xref="taxon:5693"
/clone="745"
/clone="745"
/clone="1"T, cruzi epimastigote normalized cDNA Library"
/clone=lib="T, cruzi epimastigote formalized cDNA Library"
/clone=lib="T, cruzi epimastigote"
                                                                                                                                                                                                                                                                                                                             AA890895 284 bp mRNA EST 03-APR-1998
TENS0745 T. cruzi epimastigote normalized cDNA Library Trypanosoma
cruzi cDNA clone 745 5', mRNA sequence.
g3017774
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Trypanosoma, Schizotrypanum.
1 (bases 1 to 284)
Verdun, R.E., Di Paolo, N.C., Rondinelli, E., Frasch, A.C.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene discovery through EST sequencing in Trypanosoma cruzi
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac.
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                                                                            Length 265
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Pred. No. 7.20e-06;
0; Mismatches 10; Indels
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                                                                                                                                                                           Score 29; DB 15;
Pred. No. 7.20e-06;
0; Mismatches 9
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/strain="Cl-Brenner"
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62
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ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

FEATURES

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/note="vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; mRNA made from human bone marrow stroma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected for average insert size >0.5 kb. Library supplied by Dr. Libin Jia (NHGR)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' | Grand Content | Fortal Content | 
                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 336.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA620322 379 bp mRNA EST 14-OCT-1997 af06906.s1 Soares testis NHT Homo sapiens cDNA clone 1030906 3',
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 371.
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(bases 1 to 379)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S Krizman,D., Kucaba,T., Lacy,M., Le,N., Lenon,G., Marra,M., Theising,B., White,Y., Wylie,T., Waterston,R., Tan,F., WashG-NCI human EST Project
Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Pred. No. 7.20e-06;
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/clone_11b="Jia bone marrow stroma"
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69 c 50 g 110 t
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/organism="Homo sapiens"
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larity 78.7%;
Conservative
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AA620322
g2524261
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DEFINITION
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1 (bases 1 to 369)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.
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ag39h07.sl Jia bone marrow stroma Homo sapiens cDNA clone 1119229
3', mRNA sequence.
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Enkaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

1 (bases Catarrhini, Hominidae; Homo.

Jia,L., Wilkin,D., Bittner,M., Robey,P., Young,M., Yamada,Y.,

Krizman,D., Liotta,L., Bonner,R., Schuler,G., Boguski,M.,

Powell,J., Lennon,G., Roodman,D., Hotchkiss,R., Meltzer,P.,

Trent,J., Hillier,L., Allen,M., Bowles,L., Geisel,S., Kucaba,T.,

Marra,M., Martin,J., Steptoe,M., Tan, F., Thelsing,B., Bowers,Y.,

Waylle,T., Waterston,R., Wilson,R. and Francomano,C.
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Best Local Similarity 82.2%; Pred. No. 7.20e-06;
Matches 37; Conservative 0; Mismatches 8; Indels
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/clone_11b="NGI_CGAP_GCB1"
/tissue_type="germinal center B cell"
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Seg primer: -40ml3 fwd. ET from Amersham
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WashU-MGB/NHGRI EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                     Unpublished (1997)
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Homo sapiens
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BASE COUNT

ORIGIN

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LOCUS DEFINITION

ACCESSION

ORGANISM

KEYWORDS SOURCE

REFERENCE

AUTHORS

TITLE JOURNAL COMMENT

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Gaps ö

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606" /clone="1030906" /clone="1030906" /clone="1030906" /sex="male" /sex="male" /sex="male" /sex="male" /lab_host="DH10B"
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                                                                                                                                                                                                                                                                   Score 29; DB 10; Length 379;
Pred. No. 7.20e-06;
1; Mismatches 9; Indels
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2.3%;
Best Local Similarity 78.7%;
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